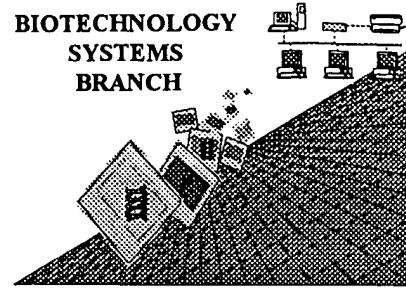


A. Guitto

RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



SHL

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/423,545A

Art Unit / Team No.:

1653

Date Processed by STIC:

3/29/2000

RECEIVED
TC 1500 MAIL ROOM
FEB 12 2001

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/423,545A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

1010
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APR 12 2000
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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545ADATE: 03/29/2000
TIME: 15:44:28

Input Set: I423545A.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

1 <110> Kenji SHIBATA
 2 Motoo YAMASAKI
 3 Tetsuo YOSHIDA
 4 Tamio MIZUKAMI
 5 Akeo SHINKAI
 6 Hideharu ANAZAWA
 7 <120> Peptides having a cyclic structure and restoring the
 8 activities of P53 protein to mutant P53 protein
 9 <130> 1061
 10 <140> US/09/423,545A
 11 <141> 1999-11-12
 12 <150> JP97/126113
 13 <151> 1997-05-15
 14 <160> 32

 Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

 (See item 1 on
 Error Summary Sheet)

E--> 15 <210> 8
 16 <211> 32
 17 <212> DNA
 18 <213> Artificial Sequence
 19 <220>
 20 <223> Other nucleic acid Synthetic DNA
 21 <400> 8

E--> 22 CTAGACAGCC AGACTGCCTT CCGGGTCACT GC 32

E--> 24 <210> 9
 25 <211> 32
 26 <212> DNA
 27 <213> Artificial Sequence
 28 <220>
 29 <223> Other nucleic acid Synthetic DNA
 30 <400> 9

E--> 31 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT 32

E--> 33 <210> 10
 34 <211> 26
 35 <212> DNA
 36 <213> Artificial Sequence
 37 <220>

Per new sequence rule,
 bases must be in
lower-case
letters

format error

32

32

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545ADATE: 03/29/2000
TIME: 15:44:28

Input Set: I423545A.RAW

38 <223> Other nucleic acid Synthetic DNA
 39 <400> 10
 E--> 40 TCGAGAGACA TGCCTAGACA TGCCTG
 41 26

42 <210> 11
 E--> 43 <211> 26
 44 <212> DNA
 45 <213> Artificial Sequence
 46 <220>
 47 <223> Other nucleic acid Synthetic DNA
 48 <400> 11
 E--> 49 TCGACAGGCA TGTCTAGGCA TGTCTC
 50 26

51 <210> 12
 E--> 52 <211> 22
 53 <212> DNA
 54 <213> Artificial Sequence
 55 <220>
 56 <223> Other nucleic acid Synthetic DNA
 57 <400> 12
 E--> 58 TCGAGCCGG GGGTACCGCA TG
 59 22

60 <210> 13
 E--> 61 <211> 14
 62 <212> DNA
 63 <213> Artificial Sequence
 64 <220>
 65 <223> Other nucleic acid Synthetic DNA
 66 <400> 13
 E--> 67 CGGTACCCCC GGGC
 68 14

69 <210> 14
 E--> 70 <211> 32
 71 <212> DNA
 72 <213> Artificial Sequence
 73 <220>
 74 <223> Other nucleic acid Synthetic DNA
 75 <400> 14
 E--> 76 TCGAGGGAACT TGCCTGGACT TGCCTGTCGA CG
 77 32

78 <210> 15
 E--> 79 <211> 32
 80 <212> DNA
 81 <213> Artificial Sequence
 82 <220>

same
format
now

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545ADATE: 03/29/2000
TIME: 15:44:28

Input Set: I423545A.RAW

83 <223> Other nucleic acid Synthetic DNA
84 <400> 15
E--> 85 *same*
86 32

87 <210> 24
E--> 88 <211> 16 *15 shown*
89 <212> PRT
90 <213> Artificial Sequence
91 <220>
92 <221> BINDING
93 <222> (7)..(13)
94 <223> BINDING type is -CONH2-.
95 <220>
96 <221> SITE
97 <222> (15)
98 <223> Xaa represents L-Leucine amide.
99 <220>
100 <223> Synthetic peptide
101 <400> 24

W--> 102 Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser Arg His Lys Lys Xaa
103 1 5 10 15

*more amino acid nos. directly under
amino acids*

✓ FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I423545A.RAW

Line	?	Error/Warning	Original Text
16	E	Input 32, Calc# Bases 0 differ	<211> 32
22	E	Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E	Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E	Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E	Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
25	E	Input 32, Calc# Bases 0 differ	<211> 32
31	E	Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E	Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E	Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E	Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
34	E	Input 26, Calc# Bases 0 differ	<211> 26
40	E	Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCTG
40	E	Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCTG
40	E	Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCTG
43	E	Input 26, Calc# Bases 0 differ	<211> 26
49	E	Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
49	E	Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
49	E	Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
52	E	Input 22, Calc# Bases 0 differ	<211> 22
58	E	Wrong Amino Acid Designator	TCGAGCCCGG GGGTACCGCA TG
58	E	Wrong Amino Acid Designator	TCGAGCCCGG GGGTACCGCA TG
58	E	Wrong Amino Acid Designator	TCGAGCCCGG GGGTACCGCA TG
61	E	Input 14, Calc# Bases 0 differ	<211> 14
67	E	Wrong Amino Acid Designator	CGGTACCCCC GGGC
67	E	Wrong Amino Acid Designator	CGGTACCCCC GGGC
70	E	Input 32, Calc# Bases 0 differ	<211> 32
76	E	Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCTGTCGA CG
76	E	Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCTGTCGA CG
76	E	Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCTGTCGA CG
76	E	Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCTGTCGA CG
79	E	Input 32, Calc# Bases 0 differ	<211> 32
85	E	Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E	Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E	Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E	Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
88	E	Input 16, Calc Seq.Length 15 differ	<211> 16
102	W	"N" or "Xaa" used: Feature required	Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser A